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Page 2

Figure 11 shows a sequence alignment made from a structural overlay of pharmacofamily 1. Amino acids shown correspond to those which are within regions that overlap in the structural overlay. All bolded letters are within 4.5 Angstroms from a ligand binding site. Underlining indicates proximity to a cofactor ligand and/or substrate ligand as follows: bold underling indicates proximity to a bound cofactor, double underling indicates proximity to a bound substrate, and dotted underling indicates proximity to both bound cofactor and bound substrate. The sequences shown are 1AGN (SEQ ID NO:1), 1AXE (SEQ ID NO:2), 1YKF (SEQ ID NO:3), 1HYH (SEQ ID NO:4), 1LDN (SEQ ID NO:5), 1EMD (SEQ ID NO:6), 9LDB (SEQ ID NO:7), 4MDH (SEQ ID NO:8), 1BMD (SEQ ID NO:9), 1PSD (SEQ ID NO:10), 1DXY (SEQ ID NO:11), 2NAD (SEQ ID NO:12), 1A4I (SEQ ID NO:13), 1B3R (SEQ ID NO:14), 1PJC (SEQ ID NO:15), 1ARZ (SEQ ID NO:16) and 1QR6 (SEQ ID NO:17).

#### REMARKS

Pages 1 through 12 are submitted herewith containing Sequences 1 through 17, formatted in accordance with the conventions set forth by PatentIn. The newly submitted pages and amendments merely identify the sequences originally set forth in the application and do not add new matter. Accordingly, entry of these amendments and pages is respectfully requested.

A marked up copy of the amended paragraphs of the specification is attached hereto as Appendix A. Language to be